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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2006, 01:24:56 ; Search time 10737 Seconds
(without alignments)
7655.902 Million cell updates/sec

Title: US-10-776-211-1
Perfect score: 1470
Sequence: 1 atgcactcaagcagagaaga.....accattcaaaaaaaaaaaaaa 1470

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

							%
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	1370.4	93.2	1426	4	CD014078	CD014078 90137769	
2	1300.6	88.5	1469	6	CR858591	CR858591 Pongo pyg	
3	1043.8	71.0	1415	4	CD014077	CD014077 90134646	

rnpb
ent pub

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OM nucleic - nucleic search, using sw model

Run on: September 29, 2006, 01:46:56 ; Search time 332 Seconds
(without alignments)
8170.456 Million cell updates/sec

Title: US-10-776-211-1
Perfect score: 1470
Sequence: 1 atgcactcaagcagagaaga.....accattcaaaaaaaaaaaaaa 1470

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2370645 seqs, 922650133 residues

Total number of hits satisfying chosen parameters: 4741290

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
	1	1468.4	99.9	1470	6	US-10-700-439-68 Sequence 68, Appl
	2	1301.4	88.5	4080	8	US-11-266-748A-23177 Sequence 23177, A
	3	1301.4	88.5	4080	8	US-11-266-748A-61067 Sequence 61067, A
	4	1275.6	86.8	2485	8	US-11-266-748A-28678 Sequence 28678, A
	5	1250	85.0	1624	8	US-11-266-748A-369502 Sequence 369502,
	6	1250	85.0	1624	8	US-11-266-748A-389190 Sequence 389190,
c	7	1250	85.0	1624	8	US-11-266-748A-452881 Sequence 452881,

OM nucleic - nucleic search, using sw model

Run on: September 29, 2006, 01:34:25 ; Search time 301 Seconds
(without alignments)
9137.973 Million cell updates/sec

Title: US-10-776-211-1
Perfect score: 1470
Sequence: 1 atgcactcaagcagagaaga.....accattcaaaaaaaaaaaaaa 1470

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1468.4	99.9	1486	4	US-09-880-107-2243	Sequence 2243, Ap
2	1312.8	89.3	2532	4	US-09-880-107-3673	Sequence 3673, Ap
3	1297	88.2	1450	4	US-09-880-107-2248	Sequence 2248, Ap
4	1276	86.8	1618	3	US-09-347-878-55	Sequence 55, Appl
5	811	55.2	899	3	US-09-949-016-3096	Sequence 3096, Ap
6	612.8	41.7	2032	3	US-09-949-016-5008	Sequence 5008, Ap
7	611.2	41.6	2048	3	US-09-949-016-106	Sequence 106, App

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OM nucleic - nucleic search, using sw model

Run on: September 29, 2006, 00:56:39 ; Search time 983 Seconds
(without alignments)
10426.455 Million cell updates/sec

Title: US-10-776-211-1
Perfect score: 1470
Sequence: 1 atgcactcaagcagagaaga.....accattcaaaaaaaaaaaaaa 1470

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB ID	Description
	Score				
1	1470	100.0	1470	13 ADT62713	Adt62713 cDNA enco
2	1468.4	99.9	1470	12 ADJ75075	Adj75075 Marker ge

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OM nucleic - nucleic search, using sw model

Run on: September 29, 2006, 01:07:11 ; Search time 8168 Seconds
(without alignments)
11508.657 Million cell updates/sec

Title: US-10-776-211-1
Perfect score: 1470
Sequence: 1 atgcactcaagcagagaaga.....accattcaaaaaaaaaaaaaa 1470

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	1468.4	99.9	1470	2	CQ776641		CQ776641 Sequence
2	1468.4	99.9	1486	2	AX330194		AX330194 Sequence

rnpbm

fat pul

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OM nucleic - nucleic search, using sw model

Run on: September 29, 2006, 01:41:52 ; Search time 1995 Seconds
(without alignments)
9054.047 Million cell updates/sec

Title: US-10-776-211-1
Perfect score: 1470
Sequence: 1 atgcactcaagcagagaaga.....!...accattcaaaaaaaaaaaaaa 1470

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1470	100.0	1470	9 US-10-776-211-1	Sequence 1, Appli

agkcm